

the contribution of year classes. Furthermore, the migratory movements of year classes appear to be time dependent. Estimates of the composition of the coastal populations are sample dependent. The size composition of the sample and the segment of the migratory population sampled (early, middle, or late migrating bass) will contribute to observed changes in the overall relative composition of the population.

DELINEATION OF KING MACKEREL (Scomberomorus cavalla) STOCKS ALONG  
THE U.S. EAST COAST AND IN THE GULF OF MEXICO

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King mackerel are widely distributed along the U.S. south Atlantic coast and in the Gulf of Mexico where they support both recreational and mixed-gear commercial fisheries. Because catches are landed within the boundaries of eight states, two regional fishery management jurisdictions and Mexico, management of the fisheries is a problem of both regional and international concern. Regional Fishery Management Councils (FMC) currently recognize two migratory groups for management purposes, one along the southeast U.S. coast and one in the Gulf of Mexico, with overlapping ranges in southeast Florida. To manage these fisheries most effectively it is important to know the identity of any component stocks, and how fishing mortality is distributed among them.

Biochemical (starch-gel electrophoresis) and mark-recapture techniques are being used to evaluate the stock structure of king mackerel. Preliminary results suggest that at least two breeding groups may exist; a western Gulf of Mexico group, and a second group in the eastern Gulf of Mexico and along the Atlantic coast.

Biochemical genetic data provide the strongest evidence. Analysis of allelic frequencies of peptidase using glycl-L-leucine as substrate in king mackerel from ten locations from the Gulf of Mexico and Atlantic coast indicates that fish sampled in Texas and Campeche, Mexico are significantly different from other sampling locations. These data do not confirm or refute the existence of a separate Atlantic migratory group. May's (1983) results for an additional seven sampling locations in the same geographic area are concordant.

Historical mark-recapture studies in the Gulf of Mexico have shown movement from south Florida in winter to the northwestern and western Gulf in summer, as well as the reverse. However, our mark-recapture data on large king mackerel tagged in winter off Louisiana suggest that these fish may comprise a different group from fish that have migrated between the western and northwestern Gulf and south Florida. Of 1,513 fish tagged and released off Grand Isle, LA, in the winters of 1983, 1984, and

1985, 31 have been recaptured, all in the western Gulf of Mexico (Louisiana, Texas, and Mexico). Thus, if two groups exist, as our results suggest, mixing of the two groups may be occurring in the western and northwestern Gulf of Mexico in summer.

Biochemical (starch-gel and isoelectric focusing electrophoresis), mark-recapture and morphological studies designed to define king mackerel stocks more precisely are continuing at the National Marine Fisheries Service Laboratory in Panama City, Florida.

#### DIFFERENTIATION OF MITOCHONDRIAL DNA IN ATLANTIC HERRING

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The relationships among spawning stocks of Atlantic herring (Clupea harengus harengus) are problematical. Recent studies have advanced the hypothesis that specific environmental attributes essential for growth and survival of larval herring largely determine where herring will spawn. Further, timing of spawning has been hypothesized to be a function of the time necessary for completion of larval growth and metamorphosis constrained by resources within the larval retention area. Implicit in this model is the idea that individual herring belong to defined groups which home to specific spawning sites, i.e., stocks. If this is the case, there should exist high genetic continuity (and identity) among individuals within stocks and relatively lower continuity among stocks. Allozyme investigations have not supported this prediction; despite the availability of a large number of polymorphic markers, genetic heterogeneity among groups is not evident. To examine further genetic relationships among herring stocks, we examined restriction endonuclease cleavage patterns of mitochondrial DNA among three spawning groups in the northwestern Atlantic.

Three discrete samples of spawning Atlantic herring were obtained: fall spawners (Jeffries Ledge, Massachusetts, southern Gulf of Maine; Trinity Ledge, New Brunswick, northern Gulf of Maine) and spring spawners (Gulf of St. Lawrence, New Brunswick). For comparative purposes, spring spawning Pacific herring (Clupea harengus pallasii) were obtained from Puget Sound. MtDNA was extracted from eggs and prepared by rapid phenol extraction and occasionally CsCl ultracentrifugation. Samples were digested with 16 six-base restriction endonucleases and restriction fragments visualized with ethidium bromide after agarose electrophoresis.

Based on cleavage patterns for 14 restriction enzymes, the size of mtDNA was estimated to be 17097 + 128bp in Atlantic herring and 16754 + 173bp in Pacific herring; intraspecific size difference was non-significant. The 294 restriction fragments observed encompassed

# **PROCEEDINGS OF THE STOCK IDENTIFICATION WORKSHOP**

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